AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. - 19. (cancelled)

20. (currently amended): A method for identifying a candidate protein useful as an anti-infective, comprising:

(a) calculating computationally protein sequence-based attributes from protein sequences of a pathogenic organism, wherein said protein sequences are predicted either from whole genomic sequences, or from partial genomic sequences comprising at least one chromosome, and wherein said protein sequence-based attributes comprise: percentage of charged amino acids, percentage hydrophobicity, distance of protein sequence from a fixed reference frame, measure of dipeptide complexity, and measure of hydrophobicity from a fixed reference frame, and wherein said pathogenic organism is selected from the group consisting of *B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae ;*

(b) clustering computationally said protein sequences based on said protein sequence based attributes using Principle Component Analysis;

(c) identifying computationally outlier proteins sequences, wherein said outlier proteins sequences appear outside a main cluster;

(d) comparing said outlier protein sequences ~~with protein sequences in databases of~~ of a group of pathogenic organisms consisting of B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae to identify outlier proteins that are unique to said pathogenic

organism based on the sequences in the databases accessed for the comparing, and to identify outlier proteins that are homologous or identical to proteins known to be involved in virulence; and

~~(e) selecting an outlier protein identified in step (d) for further testing as an anti-infective; and~~

~~(f) validating the outlier protein selected in step (e) as an anti-infective.~~

(e) displaying the results of said step (d).

21. (Canceled).

22. (previously presented): The method of claim 20, wherein said protein sequence based attributes comprise fixed protein attributes and variable protein attributes.

23. (previously presented): The method of claim 22, wherein a variable protein attribute is a distance of protein sequence from a variable reference frame.

24. (previously presented): The method of claim 20, wherein said clustering is done by Principle Component Analysis using correlation coefficient between said protein sequence based attributes.

25. (Canceled)

26. (currently amended): The method of claim 20, wherein the outlier protein ~~selected in step (e)~~ identified in step (d) is non-homologous to known anti-infective proteins from a pathogen selected from the group consisting of B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N. meningitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae.

27. (currently amended): The method of claim 20, wherein the outlier protein ~~selected in step (c)~~ identified in step (d) has an amino acid sequence selected from the group consisting of SEQ ID Nos: 1-31.

28. (currently amended): The method of claim 20, wherein the outlier protein selected in step (c) identified in step (d) has an amino acid sequence selected from the group consisting of SEQ ID Nos: 32-118.

29. (previously presented): The method of claim 20, wherein steps (a)-(c) are performed by a computer system comprising:

(1) a central processing unit (CPU), wherein said CPU executes a program that calculates protein sequence-based attributes, wherein said protein sequence-based attributes comprise: percentage of charged amino acids, percentage hydrophobicity, distance of protein sequence from a fixed reference frame, measure of dipeptide complexity, and measure of hydrophobicity from a fixed reference frame; and clusters protein sequences based on said protein sequence-based attributes using Principle Component Analysis, thereby producing results;

(2) a memory device accessed by said CPU, wherein said memory device stores said results;

(3) a display on which said CPU displays said results in response to user inputs; and

(4) a user interface device.

30. - 33. (Canceled).